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F	OR.	OFF	ICIAL	USE	ONL	Y

ACCESS DB # 153572
PLEASE PRINT CLEARLY

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0 0 5 -	Scientific and	Technical Informati	on Center		
CRFE	SEARCH	REQUEST I	FORM		
Requester's Full Name: _Art Unit: _1635 Location (Bldg/Room#): _2\[************************************	TERRA G1885 Phone Number: 2-0 10	758 Seria	#: 7953 _{Da} al Number: 10/60 nat Preferred (circle):) 5,337 PAPER D	ISK
To ensure an efficient and qual	ty search, please attach a cop	by of the cover sheet, claim	s, and abstract or fill out	the following:	1119
Title of Invention:	· · · · · · · · · · · · · · · · · · ·	· · · · · · · · · · · · · · · · · · ·			/
Inventors (please provide fu	Il names):			61	
Earliest Priority Date:				D: 38	
Search Topic: Please provide a detailed stateme elected species or structures, key Define any terms that may have a	vords, synonyms, acronyms, a	nd registry numbers, and c	ombine with the concept o		
I am not sure	if this can b		e sequence ~	1250 bg in	· length
poplicants have 8	rovided this BI	AST search wi prison	th a result	of somplet	ee Query.
83%. identity	9		,	22:518	0
I need H	re Same Comparis	ion with a '	result of 90% -	. ideuti-	ty
with SEa.	ID No: 2 (min	deobases 1715	-2060) as 1	Exhibit B	Shous !
+	V USSN	10/005,337			

2. I also need the same comparison with a result of 93% identity with SED TO MO: 1 MA - 3358 - 2 His is confusing)

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Terra,

Seg! has 100% local similarity with "Query!".

Seg! is much longer than Query!, so the overall query

match is low & can't be improved significantly.

I tried 8 different sets of parameter changes (altering Gap penalty & for Gap size penalty) to get the best match between Seg 2, nt 1715 - 5066 vs Query 1. The best I could a come up with was 82.5% Best Local Similarity (green tab).

Please let me know if you have guestions.

Barb

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Copyright (c) 1993 - 2005 Compugen Ltd.
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RESULT 2
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à g Search completed: May 25, 2005, 16:32:24 Job time : 1 secs

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Compugen Ltd.
GenCore version (c) 1993 - 2005
           Copyright
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- nucleic search, using sw model OM nucleic

ü : Run

May 25, 2005, 16:34:51

// Search time 0.872041 Seconds
(without alignments)
1.822 Million cell updates/sec

US-10-005-337A-1-COPY 2358 Title: Perfect score:

.....caggtcggaggccaccatgg 2358 1 ggatcctttcatgtttaaca Sequence:

IDENTITY_NUC Gapop 10.0 Scoring table:

1 segs, 337 residues Searched: Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 seq seq 88 08 08 Minimum Maximum

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

new.seq:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Entered (bobryen Entered (bobryen Description QUERY 1 П - -DB 337 Query Match Length 14.3 0.9 337 Score 4 0 Š.

ALIGNMENTS

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OUERY 1 ; Entered [bobryen 25-May-05 16:13] QUERY 1

Gaps . 0 Length 337; 0; Indels DB 1; Query Match
14.3%; Score 337; DB
Best Local Similarity 100.0%; Pred. No. 0;
Matches 337; Conservative 0; Mismatches 1972 GCAATATTAACAGGCAGCTGTCCCCTGGCTTCCCGATACGTGGGATGACTCGCATTGCTG

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CGCGGCCAGCTTGTCATCTCCCTCTTGGGCTTCCCAGACACTAAGTCTGGAATGAAATT 2151

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241 AAGATTATCTCACCCAGCCCTAGCTATATAACGGGCTGGTGGGAGGGCTCCACAGGGC 300 CAGTICCAGGGGTICATCCACAAGAGAAAAACATA 2308 CAGTTCCAGGGTTCATCCACAAGAGAAAAACATA 337 2272 301 셤 ò g

RESULT 2 QUERY 1/c ; Entered [bobryen 25-May-05 16:13] QUERY_1

ū, 610 670 790 266 671 AGATCCTTGGCCTTGAATTAGGGAGGCACAAAATACTCAGAGATTCAAGACTGCTC 730 197 850 -----AATTCAGAGGCAGGTGAATTTTCATTCCAGACTTAGTGTCTCGGAAGCC 148 911 ATAGCGTCTCAGGACAGATAGGACAGAGAGAACACTAGGAGAGGGGAACCCACGAAGGAC 970 611 CTCTGCATCCATAGCAAGTAGCCTAATGTTTTCTGTGTCTAGGTGTCATCTCTGTGAATCG 731 AGCAGCCCAGAGTCCTTCCTCAAAGGAAAGGTCTCAAACTCTCAGCCCCCCTTAGCTCTGA -----ricagiciagadagicaagicaagicacagicacagicacagicagicagi TCTTATGGGTGGAGCCAAGACGCATCGTGGGTGGAGCGAAGACGCAACCTCACCTTCTAG CAAGAGGTCAAAGAAAATAGTGTTAACCATGAAAACGAGAAGACCAACAGTTATCCATTG 325 retrieredatedaceceredaactegecerefedadececeredacedecegriatar 791 GTCAGGCCTGGAACAAACGGCCACAGGAATGAGAAAAGCTGCCATAGCTGCTTGTCACTT Gaps Indels 1186; Length 337; 0; Mismatches 151; Score 21.4; DB 1; Pred. No. 0; 265 AGCTAGGGCTGGGTGAGATAATCT---0.9%; Matches 162; Conservative Similarity 851 551 241 196 241 Query Match Best Local ઠે 임 ò ద ઠે 셤 ઠ g ઠે ద ð 요 ò

971 AAGGTATTAGTGTTGGTTTTTCAGGGCAATGTCTTGTACTGAAGATTCTAGAAACACAA 1030 1031 TTTGCTGGTTGAACAGCTGAAGTGGGGTGGGGGTTCTTACCCCATGTTCATGGAAGGGTG 1090 1151 CACTTCCCTCTTCTACTGACACCCCCTTCACTCTCCTTTCATAAAAAATAAAAAGT 1210 1211 ATTTTATGTGGCTCTTACGATAGAATCTTTCCTCGAACTATAAAAAGATCTAAAATATTTA 1270 131 1271 TATTTTTCACATTTTAATATCTTAGCGATGACAAGCCAGAAACAAGTATTTTTGCCTCT 130 130 130 130 130 ઠે g ઠે g ð g ઠે g ò 셤 ò 쉽

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Db 100	101	
Qy 1511	TTGTGCTTCTGCTAAGAACTGGACTCACATCTCTGTGCATCACTTCGGCCCGTTTTGG 1570	
0D 100	101	f
Oy 1571	GGTAGATCCTCTGATTAGCCTTCAGATTTAGAACACGGTGAGCCTGTGGTGCACTAATTA 1630	Kesur
Db 100	101	; ; ; ;
Qy 1631	TGGCCAGTGACACCATAGAGTCAAAGTGCATTACTGAATGCTTTCAATTTCTCCTAATGC 1690	υ
Db 100	101	
Qy 1691	TGGTACGATGGCATGTCACAGGGCCATTTTAGCTGCAGACATCACTCCAGAGAATTCCAA 1750	11000
Db 100	AATGTGAGGGTCATTCCTTTGGCAGGTGACCACACC 64	QUERY
Qy 1751	ACAGATAGAGACAAGGGCACCCAGACCCATCTCCCTCGGGCTGATTATCCCCCAG 1810	QUERY
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Qy 1811	AAATAGGATGTCCCAAAGCAACACTTCCCAGCCAACTGGAGTGCTGATAAGTCCAGTTAT 1870	Mat
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Qy 1871	CAGAAAGATATGGCTGTAAGTGTGATGCACAGTGCTTGCATTTTCTTGATACGTTAGTCA 1930	අු
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Oy 1931	TATGAGAGCTGACAAAGAAGAAAAAAGAGCAGCGATGTGGTGCAATATTAACAGGCAGCT 1990	qq
Db , 63	64	λõ
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Db 63	GCTCAGCAATGCGAGTCATCCCACGTATCGGGAAGCCAGGGGACAGCTGCC 13	<i>\d</i>
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Maximum Match 100%
Listing first 45 summaries
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new.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Entered [bobryen Entered [bobryen			337; 8; Gaps 4;		rcecarrecre 60	NTTCACATATTC 119	vřiceckíkoec 120	GTCTGGAATGA 179			SGAGGGCCCAG 299	GAGGGCTCCA 294		
Desc	Ent	NTS		2; DB 1; Length 0; ches 58; Indels	GCAATGTCAACAGACAGCTGTCCCCTGAC-TCTTGACAAATAGGATGAC	<u>ĠĊAĂTATTAAĊAGGCAĞCTĞTCCCCTGGCTTCCCGATACGTGGGGATGACTCGCATTGCTĞ</u>	AGGATGTGATCACCACCAAGGAATGGCCCTCTCACATTTCTTCCTGATTCACATATTC	<u> Adcigardacidacidacida Adgia Adcida Carcacida Tricar Trogonia Cocaracida Cocara Cocar</u>	AGCAGGGTIAGCTIGICCTCCCTCCTTCAGCTITCCCAGACACIGAGTCTGGAATGA	AAATTCACCTGCCTCTGAGTTGGCTCCTAATGGGGGGGGG		GTTGGAAGATTATCTCACCCGGCCCCAGCTATATAAGCTGACGGTGTGGAGGGCCCAG	GCTGGAAGATTATCTCACCCCAGCCCTAGCTATATAA-CGGGCTGGTGTGGAGGGCTCCA	CAGGGCCAACTCCAGGGATTCCTTC-CACGACAAAAACATA 341	chgggccagtrcaggggttcatccacaagagagaaaaacata 337
ΩI	QUERY 1 QUERY_1	ALIGNMENTS	16:13]	Score; Pred.	CTGTCCCCTGAC	crercccreec	CAAAGGAATGGC	caaaggaargac	CTCCCTCCCTC	AGTTGGCTCCTA	 AATTGGCCACTG	CCCGGCCCCAGC	CCCAGCCCTAGC	ATTCCTTC-CAC	gricarcada
Length DB	337 1			58.4%; larity 80.8%; Conservative	AACAGACAG	AACAGGCAG	GATCACCAC	dercacrec	TAGCTTGTC	CTGCCTCTG	CTGCCTCTG	ATTATCTCA	ATTATCTCA	ACTCCAGGG	GTTCCAGG
* Query Match	58.4		[bobryen 25-May-05	겯	CAATGTO	caararı	GCGATGI	decerrer	AGCAGGGT	AATTCAC	AATTCAC	TTGGAAG	CTGGAAG	AGGGCC?	AGGGCCA
Score	202.2			atch cal	г Б	1 G	60 A	61 A	A 120		176 A	240 G	236 G	300	295 0
Result No.	c 2		RESULT 1 QUERY_1 ; Entered QUERY_1	Query Match Best Local Matches 27	λ̈́O	Dp	ò	qq	٠ ک ا	3 8	· A	à	qa	'n	Db

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lery Match
4.3%; Score 15; DB 1; Length 337;
set Local Similarity 26.7%; Pred. No. 0;
atches 62; Conservative 0; Mismatches 45; Indels 125; Gaps

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205 CCTAATGGGGGGGGGGGGTTTTCGGTTCCCAGGTTGGAAGATTATCTCACCCGGCCC 264

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Search completed: May 25, 2005, 16:34:53 Job time: 0.127959 secs

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Maximum DB E
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(without alignments)
1589.292 Million cell updates/sec
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Compugen Ltd
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14.3%; Score 337; DB
Best Local Similarity 100.0%; Pred. No. 0;
Matches 337; Conservative 0; Mismatches
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version 5 - 2005 (
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Maximum Match 100%
Listing first 45 summaries
                                                         - nucleic search, using sw model
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GenCore (c) 1993
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2358
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QUERY_1
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Result

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2114 TCTTGGGCT-TCCCAGACA--CT--AAGTCTGGAATGAAATTCA----CCTG-CCTCTG 2163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2223 AATTGGCCACTGGTGGGGGCAGGGGTGTGACTTGGCTTCCCAGGCTGGAAGATTATCTCA 2223
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241 AAGATTATCTCACCCAGCCCTAGCTATATAACGGGCTGGGTGTGGGAGGGCTCCACAGGGC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 AGAGGGTCATTCCTTTGGCAGTGACCACACG-CTC-AGCAAT-GCGAG--T-CAT-CCC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (without alignments)
233.204 Million cell updates/sec
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53.8%; Pred. No. 0;
iive 0; Mismatches 107; Indels
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Copyright (c) 1993 - 2005 Compugen Ltd
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                                                                                      CAGTTCCAGGGTTCATCCACAAGAGAAAAACATA 2308
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346
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QUERY 1/c
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QUERY_1
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seq length: 200000000
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Matches 170; Conservative
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Database :
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	Description	Entered [bobryen Entered [bobryen
SUMMARIES		
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	Query Match Length DB ID	337 1 QUERY 1 337 1 QUERY 1
æ	Query Match	69.0
	Score	238.8 69.0 36.8 10.6
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ALIGNMENTS

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		GCAATGTCAACAGACAGCTGTCCCCTGAC-TCTTGACAAATAGGATGACTTGCATTGCTG	GCAATATTAACAGGCAGCTGTCCCCTGGCTTCCCCÄTACGTGGGATGACTCGCATTGCTG	AGGGATGTGATCACCACAAAGGAATGGCCCTCTCACATTTCTTCCTGATTCACATATTC	AGCGGTGTGTGTCACTGCCAAAGGAATGACCCTCTCACATTTCTTCTTCTGATTCGCATACGC	AGCAGGGTTAGCTTGTCCTCCCTCTTCAGCTTCCCAGACACTGAGTTGGATGA	-CTCCCTCTTGGCTTCCCAGACACTAAGTCTGGAATGA	AAATTCACCTGCCTCTGAGTTGGCTCCTAATGGGGGGGGG	AAATTCACCTCTCTGTAATTGGCCACTGGTGGGGGGCAGGGTGTGTGT	GTTGGAAGATTATCTCACCCGGCCCCAGCTATATAAGCTGACCGGTGTGGAGGGCCCAG	GCTGGAAGATTATCTCACCCAGCCCTAGCTATATAA-CGGGCTGGTGTGTGTTCCCA	CAGGGCCAACTCCAGGATTCCTTC-CACGACAGAAAACATA	CAGGCCCAGTTCCAGGGTTCATCCACAAGAGAAAAAATA
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RESULT 2
QUERY 1/c

DEST 1/c

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QUERY_ ò

24; 319 GGATGAACCCCTGGAA--CTG-GCCCTGTGGAGCCCCTCCACACCA--GCCC-GTTATA 267 98 TITCT--TCCTGATTCACATA---TT-CAGCAGGGTTAG-CTTGTC-CTCCCCT-CCCTC 148 149 TTCAGCTTCCCAGACACTGGAATGAAAATTCA--CCTGCCTCTGAGT-TGG--C 203 206 ACCAG-TGGCCA-ATTCAGAGGCAGG--TGAATTTTCATTCCAGACTTAGTGTCTGGGAA 151 97 42 GGATGA---CTTGCATTGCTGAGCGATGT-GATCACCAAAGGAATGGCCCTCTCACA Query Match 10.6%; Score 36.8; DB 1; Length 337; Best Local Similarity 55.3%; Pred. No. 0; Matches 146; Conservative 0; Mismatches 82; Indels 36; Gaps qq ò g ઠ

204 TCCTAATGGGGGGGGAG-TG-TTACTTCG--GT-TCCCAGGTTGGAAGATTATCTCACC 258 150 gcccaagaggagargacaagcrgccgcggggrargcgaarcaggaagaa-argrgaga 92 g ઠે õ

259 CGGCCCCAGCTATATAGCTGACC 282 91 GGGTCATTCCTTTGGCAG-TGACC 69 셤

Search completed: May 25, 2005, 16:35:36 Job time : 1 secs

GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.

- nucleic search, using sw model nucleic

Run on:

May 25, 2005, 16:36:21 ; Search time 0.872041 Seconds (without alignments) 1.822 Million cell updates/sec

US-10-005-337A-1-COPY 2358 Title: Perfect score:

1 ggatcctttcatgtttaaca......caggtcggaggccaccatgg 2358 Scoring table: Sequence:

IDENTITY NUC Gapop $0.\overline{5}$, Gapext 0.01 segs, 337 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

new.seg:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Entered [bobryen Entered [bobryen Description QUERY 1 Ω 337 1 337 1 Query Score Match Length DB 14.3 337 No. 7

ALIGNMENTS

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RESULT 1 QUERY_1 S. Entered [bobryen 25-May-05 16:13] QUERY_1

ó; 14.3%; Score 337; DB 1; Length 337; 100.0%; Pred. No. 0; tive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 337; Conservative 1972 GCAATATTAACAGGCAGCTGTCCCCTGGCTTCCCGATACGTGGGATGACTCGCATTGCTG

2031

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Gaps

2032 AGCGGTGTGGTCACTGCCAAAGGAATGACCCTCTCACATTTCTTCCTGATTCGCATACGC 2091 120 9 GCAATATTAACAGGCAGCTGTCCCCTGGCTTCCCGATACGTGGGATGACTCGCATTGCTG AGCGGTGTGGTCACTGCCAAAGGAATGACCCTCTCACATTTCTTCTTGTTTCGCATACGC 61 셤 ò g

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2212 AAGATTATCTCACCCCAGCCCTAGCTATATAACGGGCTGGTGGAGGGGGCTCCACAGGGC 2271

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181

241 AAGATTATCTCACCCCAGCCCTAGCTATATAACGGGCTGGTGTGGAGGGGCTCCACAGGGC 300 CAGITCCAGGGGITCATCCACAAGAGAAAAACAIA 2308 301 CAGTTCCAGGGGTTCATCCACAAGAGAAAAACATA 337 2272 요 셤 ò

RESULT 2
QUERY_1/c

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QUERY_1

QUERY_1

109; 335 288 82 TTCCTAGTCTAGTCCGTTTGTGAAACTCAGCCCATCCCAACACTTCTGCAAGCCCCATCC 141 201 314 261 304 262 AGGGGTCACATATCATCTATATGTCAGGTATTTACATTACGATTCGTAACAGTAG 321 302 381 302 441 202 GGGCAGCAGTTCTCAACCTGGGGGGCCTCGACCCTTTAGGGGGGAATCAAACGACCTTTAC 22 TATCAACCCTAACCCAAGGGAACAGCCTGCCTGACAGTGGCTTTGCCACCCATGAATAC 3.7 TAT--------142 TCTACAAGGIGCICATIGGGAATTICCIGGAGCTTCTCTTTCAGGATCAGCCTGATTCTA CAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATTGAAGGTCACCACAATT -----ACCCCT-----GGAA------0; Indels 1973; DB 1; Length 337; Query Match
12.0%; Score 282.5; Best Local Similarity 14.6%; Pred. No. 0; Matches 337; Conservative 0; Mismatches 301 334 326 313 322 301 303 ઠે 유 ઠે 셤 ઠ 셤 ð 셤 ď g qq à ò ò

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922 GGACAGATAGGACAGAGAACACTAGGAGAGGGGAACCCAGAAGGACAAGGTATTAGT 981 	
982 GIGITGGITTTCAGGCCAATGTCTTGTACTGAAGATTCTAGAAACACAATTTGCTGGTTG 1041 	_
1042 AACAGCTGAAGTGGGGGGTTCTTACCCCATGTTCATGGAAGGGTGAGTGA	
ACAGATATATGATGGCCAGCATAACAAACATACACAACACCCTAATTAACACTTCCCTCT	
141 1162 TCTACTGACACCCCTTCACTCTCTTCATAAAAAAAAAAA	
CTCTTACGATAGAATCTTTCCTCGAACTATAAAAAGATCTAAATATTTATATTTTTCACA	
139 140 1282 TTTTAATATCTTAGGGATGACAAGCCAGAAACAAGTATTTTTTGCCTCTCTCAACAGCAA 1341 139AGATGACAAGC	
1342 AGCTTGGGGCCTTTTGTTTCGTGTTAGAATAGAACACGAGAGCCCGTGTATCTAGG 1401 	
1402 CAGATGCTCTATCATTAGCCCATGAGTCTCCAGCCTCAGACGCACATTTTTCTCGGGCTC 1461 	
1462 TCTTAAGCTTTTCCCACACACATTGGGAAACTTTACTGACAGCATCCAAGTTGTGCTTCTG 1521 	
1522 CTAAGAACTGGACTCACATCTCTGTGCATCACTTCGGCCCGTTTTGGGGTAGATCCTC 1581	
1582 TGATTAGCCTTCAGATTTAGAACACGGTGAGCCTGTGGTGCACTAATTATGGCCAGTGAC 1641 	
1642 ACCATAGAGTCAAAGTGCATTACTGAATGCTTTCAATTTCTCCTAATGCTGGTACGATGG 1701	
CATGTCACAGGGCCATTTTAGCTGCAGACATCCAGAGAATTCCAAACAGATAGAGA	
1762 CAAGTGGCACCCAGACCCATCTCCCTTCGGGGCTGATTATCCCCAGAAATAGGATGT 1821 65	
1822 CCCAAAGCAACATTCCCAACTGGAGTGCTGATAAGTCCAGTTATCAGAAAGATAT 1881 	
1882 GGCTGTAAGTGTGATGCACAGTGCTTGCATTTTCTTGATACGTTAGTCATATGAGAGCTG 1941 	
1942 ACAAAGAAAAAAAAAGGCAGCGATGTGGTGCAATATTAACAGGCAGCTGTCCCCTGGCT 2001	

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2062 CTCTCACATTTCTTCCTGATTCGCATACGCCGCCGAGCTTGTCATCTCCCTTTGGGC 2121
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                               2002 TCCCGATACGTGGGATGACTCGCATTGCTGAGCGGTGTGGTCACTGCCAAAGGAATGACC 2061
                                                                                                                                                                                                                                             2182 GCAGGGGTGTGACTTGGCTTCCCAGGCTGGAAGATTATCTCACCCAGCCCTAGCTATATA 2241
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1.822 Million cell updates/sec
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1 gcaatgtcaacagacagctg......gacagaaaaacatacaaga 346
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                    2302 AAACATAGACTCGAGGTCTAGGGAGCTTGC 2331
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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25; CGGTGTGGAGGGGC-CCAGCAGGGCCAACTCCAGGGATTCCTTCCAC--GACAGAAAAAC 338 53 ATTGCTGAGCGATGTGATCAC--CACCAAAGGAATGGCCCTCTCACATTTCTTCCTGATT 110 54 ATTGCTGAGCGGTGTGGTCACTGC--CAAAGGAATGACCCTCTCACATTTCTTCCTGATT 111 111 CACATATTCAGCAG-GGTTAGCTTGTCCTCCCTCCCTTCAG--CTTCCCAGACACTG 167 163 AGTCTGGAATGAAAATTCACCTCTGAGTTGGCTC-CTAATGGGGGC-GGGAGTGTT 225 221 ACTTCGG-TTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATATAA---GCTGAC 281 222 ACTT-GGCTTCCCAGGCTGGAAGATTATCTCACCCAGCCCTAGCTATATAACGGCCT--- 277 278 -dereregadedecreca-caddecearrecadederr-carceacaadadaaaac 334 53 CGCATA--C-GCCGCGGCCAGCTTGTCAT---CTCCCTCTT--GGGCTTCCCAGACACA 1 GCAATGTCAACAGACAGCTGTCCCCT-GACTCTT---GACAAATA----GGATGACTTGC Indels 48; Gaps Length 337; Query Match 75.9%; Score 262.5; DB 1; Best Local Similarity 79.9%; Pred. No. 0; Matches 290; Conservative 0; Mismatches 25; RESULT 1 QUERY 1 ; Entered (bobryen 25-May-05 16:13) QUERY 1 ATA 341 ATA 337 164 112 168 226 282 셤 ò a 셤 ઠ

RESULT 2
QUERY_1/c
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match
Best Local Similarity 45.2%; Pred. No. 0;
Bat Local Similarity 45.2%; Pred. No. 0;
Matches 208; Conservative 0; Mismatches 9; Indels 243; Gaps
Oy 4 ATG--TCAACAGACAGCTGTCCCCTGACTCTTGACAAATAGGATGA--CTTGCATTGCTG

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242 TGGAAGATTATCTCA-----CC-CGGCCCCAGCTATATAAGCTGA--CCGG-----TG 286

Search completed: May 25, 2005, 16:36:23 Job time: 0.127959 secs

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Best Local Similarity
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                                                                                          May 25, 2005, 16:37:10 ; Search time 0.872041 Seconds (without alignments)
1.822 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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241 AAGATTATCTCACCCAGCCCTAGCTATATAACGGGCTGGTGTGGAGGGGCTCCACAGGGC 300
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                                                                                                                                                                                                                                                                                                             Score 17.4; DB 1; Length 337;
Pred. No. 0;
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al Similarity 53.7%; Pred. No. 0;
36; Conservative 0; Mismatches 31; Indels
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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ne : 0.872041 secs
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Gapop 20.0 , Gapext 0.0
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QUERY 1/c
: Entered [bobryen 25-May-05 16:13]
QUERY_1
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                                                                                                                                                                                                                                                                                                      120 AGCAGGGTTAGCTTGTCCTCCCTCCTTCTTCAGCTTCCCAGACACTGGAATGA 179
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                                                                                                                          6; Gaps
                                                                                       Query Match
49.0%; Score 169.6; DB 1; Length 337;
Best Local Similarity 75.1%; Pred. No. 0;
Matches 257; Conservative 0; Mismatches 79; Indels 6
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RESULT 2 QUERY_1/c ; Entered [bobryen 25-May-05 16:13] QUERY_1 Query Match
3.7%; Score 12.8; DB 1; Length 337;
Best Local Similarity 51.8%; Pred. No. 0;
Matches 29; Conservative 0; Mismatches 27; Indels

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Search completed: May 25, 2005, 16:37:11 Job time : 0.127959 secs

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Score
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  (without alignments)
1589.292 Million cell updates/sec
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Entered [bobryen
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14.3%; Score 337; DB 1; Length 337;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 337; Conservative 0; Mismatches 0; Indels
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                   - nucleic search, using sw model
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QUERY_1
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Gapop 60.0 , Gapext 0.0
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2358
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QUERY 1
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Maximum DB seq length: 200000000
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241 AAGATTATCTCACCCCAGCCCTAGCTATATAACGGGCTGGTGTGGAGGGGCTCCACAGGGC 300
                                                                                                                                                                                                                                                                                                                                                                                                       186 CAGGTGAATTTTCATTCCAGACTTAGTGTCTGGGAAGCCCAAGAGGGAGATGACAAGCTG 127
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233.204 Million cell updates/sec
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                                                                                                                                                                                                                                                                                 0.7%; Score 17.4; DB 1; Length 337; 53.7%; Pred. No. 0; arive 0; Mismatches 31; Indels
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(c) 1993 - 2005 Compugen Ltd.
                                                                   2272 CAGTTCCAGGGTTCATCCACAAGAGAAAAACATA 2308
                                                                                            301 CAGTTCCAGGGGTTCATCCACAAGAGAAAAACATA 337
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Maximum Match 100%
Listing first 45 summaries
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QUERY 1
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Job time : 1 secs
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Gapop 60.0 , Gapext
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QUERY_1/c
; Entered [bobryen 25-May-05 16:13]
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                                                                                                                                      22 CCCCTGACTCTTGACAATAGGATGACTTGCATTGCTGAGCGATGTGATCACCACCAAAG 81
                                                                                                                                                            23 CCCTGGCTTCCCGATACGTGGGATGACTCGCATTGCTGAGCGGTGTGGTCACTGCCAAAG 82
                                                                  Query Match 37.2%; Score 128.6; DB 1; Length 337; Best Local Similarity 73.8%; Pred. No. 0; Matches 236; Conservative 0; Mismatches 79; Indels 5; Gaps
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Query Match 3.7%; Score 12.8; DB 1; Length 337; Best Local Similarity 51.8%; Pred. No. 0; Matches 29; Conservative 0; Mismatches 27; Indels (

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Search completed: May 25, 2005, 16:37:51 Job time : 0.001 secs

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1769 CACCCAG 1775
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                                                                                                 May 25, 2005, 16:38:25 ; Search time 0.872041 Seconds (without alignments) 1.822 Million cell updates/sec
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version 5.1.6
- 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 14.3%; Score 337; DE Best Local Similarity 100.0%; Pred. No. 0; Matches 337; Conservative 0; Mismatches
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Maximum Match 100%
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Gapop 60.0 , Gapext 60.0

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GenCore (c) 1993
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2358
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QUERY_1
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1709 CAGGGCCATTTTAGCTGCAGACATCACTCCAGAGAATTCCAAACAGATAGAGACAAGTGG 1768
241 AAGATTATCTCACCCCAGCCCTAGCTATATAACGGGCTGGGGGGTGTGGAGGGGCTCCACAGGGC 300
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346
1 gcaatgtcaacagacagctg......cgacagaaaaacatacaaga 346
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                                                                                                                                                                                                                                                                                                                       Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                           2272 CAGTTCCAGGGTTCATCCACAAGAGAAAAAAAAA 2308
                                                                                                     301 CAGTTCCAGGGGTTCATCCACAAGAGAAAAAACATA 337
                                                                                                                                                                                                                                                                                                                    0.7%; Score 17.4; DB 1;
53.7%; Pred. No. 0;
tive 0; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - nucleic search, using sw model
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QUERY_1
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Job time : 0.872041 secs
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; Entered [bobryen 25-May-05 16:13]
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seq length: 200000000
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Match Length DB
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                                                                                                                                                                                                                                                                                                                               194 ATTGGCCACTGGTGGGGGGGGGGGGTGTGACTTCGCTTCCCAGGCTGGAAGATTATCTCAC 253
                                                                                                                                                                                                              138 TCCCCTCCCTCTTCAGCTTCCCAGACACTGAGAAATTCACCTGCCTCTGA 197
                                                                                                                                                                                                                                                     134 TCATCTCCCTCTTTGGGCTTCCCAGACACTAGGTCTGGGAATGAAAATTCACCTGCCTCTGA 193
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                                                                                                                                                                                                                                                                                                                                                                                                                          254 CCAGCCCTAGCTATATAACGGGCTGTGTGGAGGGGCTCCACAGGGCCAGTTCCAGGGGT 313
                                                                                                                                                                                                                                                                                                       198 GTTGGCTCCTAATGGGGGGGGGGGTGTTACTTCGGTTCCCAGGTTGGAAGATTATCTCAC 257
                                                                                                                                                                0; Gaps
                                                                                                                   Query Match 34.9%; Score 120.8; DB 1; Length 337; Best Local Similarity 74.5%; Pred. No. 0; Matches 152; Conservative 0; Mismatches 52; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           318 ITCCTTCCACGACAGAAAACATA 341
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RESULT 1
QUERY_1
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QUERY_1
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RESULT 2 QUERY 1/c Entered [bobryen 25-May-05 16:13] QUERY_1

0; Gaps Query Match 3.7%; Score 12.8; DB 1; Length 337; Best Local Similarity 51.8%; Pred. No. 0; Matches 29; Conservative 0; Mismatches 27; Indels (

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85 TGGCCCTCTCACATTTCTTCCTGATTCACATATTCAGCAGGGTTAGCTTGTCCTCC 140

ò g Search completed: May 25, 2005, 16:38:26 Job time: 0.127959 secs

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
                  Copyright
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OM nucleic - nucleic search, using sw model

Run on:

May 25, 2005, 16:39:04 ; Search time 0.001 Seconds (without alignments) 1589.292 Million cell updates/sec

US-10-005-337A-1-COPY 2358

Perfect score:

.....caggtcggaggccaccatgg 2358 1 ggatcctttcatgtttaaca. Sequence:

Gapop 0.5 , Gapext 60.0 IDENTITY NUC Scoring table:

1 segs, 337 residues Searched: Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Bed Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

new.seg:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Entered (bobryen Entered (bobryen Description QUERY_1 QUERY_1 ü 337 1 337 1 Query Match Length DB 14.3 Score 337 7 Š.

ALIGNMENTS

RESULT 1 QUERY 1 Fintered [bobryen 25-May-05 16:13] QUERY_1

Length 337; 0; Indels Query Match 14.3%; Score 337; DB 1; Best Local Similarity 100.0%; Pred. No. 0; Matches 337; Conservative 0; Mismatches 0 2031 9 1972 GCAATATTAACAGGCAGCTGTCCCCTGGCTTCCCGATACGTGGGATGACTCGCATTGCTG GCAATATTAAACAGGCAGCTGTCCCCTGGCTTCCCCGATACGTGGGGATGACTCGCATTGCTG ò

2091 2151 120 CGCGGCCAGCTTGTCATCTCCCTCTTGGGCTTCCCAGACACTAAGTCTGGAAATT 2032 AGCGGTGTGGTCACTGCCAAAGGAATGACCCTCTCACATTTCTTCCTGATTCGCATACGC 61 AGCGGTGTGGCCAAAGGAATGACCCTCTCACATTTCTTCCTGATTCGCATACGC 2092 ઠે g δ

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2212 AAGATTATCTCACCCAGCCCTAGCTATATAACGGGCTGGTGGGGGGGCTCCACAGGGC 2271

1709 CAGGGCCATTTTAGCTGCAGACATCACTCCAGAGAATTCCAAACAGATAGAGACAAGTGG 1768 241 AAGATTATCTCACCCCAGCCCTAGCTATATAACGGGCTGGGGGGTGGGGGGCTCCACAGGGC 300 186 CAGGIGAATITICATICCAGACTIAGIGICIGGGAAGCCCAAGAGGGAGATGACAAGAGCTG 127 ö Length 337; 2272 CAGTTCCAGGGTTCATCCACAGAGAGAAAAACATA 2308 301 CAGTTCCAGGGGTTCATCCACAAGAGAAAAACATA 337 Query Match 0.7%; Score 17.4; DB 1; Best Local Similarity 53.7%; Pred. No. 0; Matches 36; Conservative 0; Mismatches 31; QUERY 1/c ; Entered [bobryen 25-May-05 16:13] QUERY_1 1769 CACCCAG 1775 126 GCCGCGG 120 유 ò 셤 ઠે d 8 g

GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd. Copyright

Search completed: May 25, 2005, 16:39:05 Job time : 1 secs

- nucleic search, using sw model

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May 25, 2005, 16:39:04 ; Search time 0.001 Seconds (without alignments) 233.204 Million cell updates/sec Run on:

US-10-005-337A-2_1715-2060 346 1 gcaatgtcaacagacagctg......cgacagaaaaacatacaaga Perfect score: Sequence:

346

IDENTITY NUC Gapop $0.\overline{5}$, Gapext 60.Scoring table:

0

1 segs, 337 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post_processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Gaps

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new.seg:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	1 120.8 34.9 337 1 QUERY 1 Entered [bobryen c 2 12.8 3.7 337 1 QUERY 1
0	1 120.8 34.9 337 1 QUERY 1 2 12.8 3.7 337 1 QUERY 1
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esult Query No. Score Match Length DB ID	120.8 34.9 12.8 3.7
o.	77
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                                                                                        Score 120.8; DB 1; Length 337;
Pred. No. 0;
0; Mismatches 52; Indels 0
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QUERY 1
Entered (bobryen 25-May-05 16:13)
QUERY_1
                                                                                          Query Match
Best Local Similarity 74.5%;
Matches 152; Conservative
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0; Gaps Query Match 3.7%; Score 12.8; DB 1; Length 337; Best Local Similarity 51.8%; Pred. No. 0; Matches 29; Conservative 0; Mismatches 27; Indels RESULT 2 QUERY 1/c Finered (bobryen 25-May-05 16:13) QUERY_1

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Search completed: May 25, 2005, 16:39:05 Job time : 0.001 secs